

Appendix D

```
***** [align] *****  
options = -align -type=protein -matrix=blosum -gapdist=8 -maxdiv=40 -outorder=aligned -gapopen=10 -gapext=0.2 -pwmatrix=blosum -pwgapopen=10 -pwgapext=0.1  
CLUSTAL W (1.83) Multiple Sequence Alignments
```

Sequence type explicitly set to Protein

Sequence format is Pearson
Sequence 1: E1-A0209P-2 498 aa
Sequence 2: BAC77020 502 aa

Sequence 2: BAC77020 Start of Pairwise alignments

Aligning..

Sequences (1:2) Aligned. Score: 29

Start of Multiple Alignment

There are 1 groups:
Aligning

Aligning...
Group 1:

Group 1:
Sequence: 2 Score: 2960

Alignment Score 601

Assignment scores 60%

query.ain

CEUSTAE_W (1.83) multiple sequence alignment

E1-A0209P-2 KKK-MITQRFQLEKKPYI TAYRGGMIL LTIAI LAVDFFPI FPFRRAFKVETWGTSMLDGLV
BAC77020 VFASFLKISLESEYNPAITCYRVINSVFTAIAI LAVDFFPLFPRRAFKATELYGTGAMDFGV

E1-A0209P-2 GSFVFSNGIVSSRALLKNLNSLKSKPSFLKNAFNLAKSGGTLLFLGLRLRFFVKNLEYQEHBAC77020 GGFITFGAAMVCPEVRKK----YTEGSRFNHRLRKSLYSWVPLWFVFLGMGRVLVIKSGYQE

E1-A0209P-2 ADRN---CFFSANREG|FSFLGYCS|FLWGQNTGFYLLGNKPTLNLYKPSTQDVVAAS

E1 462200B-2 KKSTHDWYNTSHTDLSG LQJWSTLFLVYSLVYEGOYUVDYQWDRBMLWRYTWW

ET-AQ205F-2
BAC77020

BAC77020 HTGAFWTLAVLSIYMFAACLVIYVLDLQGKTIKFW
..... :: ** * ..:: * : * **:

query.ard
(E1-A0209P-2:0.35241, BAC77020:0.35241);